Page 1 of 7 4 CO

2 3/14/61

OIPE 4/3

RAW SEQUENCE LISTING

0.0

DATE: 03/19/2001

PATENT APPLICATION: US/09/781,880

TIME: 13:09:42

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03192001\I781880.raw

```
4 <110> APPLICANT: Glucksmann, Maria Alexandra
              Silos-Santiago, Inmaculada
      7 <120> TITLE OF INVENTION: Novel Seven-Transmembrane
             Proteins/G-Protein Coupled Receptors
     11 <130> FILE REFERENCE: 35800/208932
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/781,880
C--> 13 <141> CURRENT FILING DATE: 2001-02-12
     13 <150> PRIOR APPLICATION NUMBER: 60/182,061
     14 <151> PRIOR FILING DATE: 2000-02-11
     16 <160> NUMBER OF SEQ ID NOS: 10
     18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     20 <210> SEQ ID NO: 1
     21 <211> LENGTH: 1875
     22 <212> TYPE: DNA
     23 <213> ORGANISM: Homo sapiens
     25 <220> FEATURE:
     26 <221> NAME/KEY: CDS
     27 <222> LOCATION: (323)...(1522)
     29 <221> NAME/KEY: misc_feature
     30 <222> LOCATION: (1)...(1875)
     31 <223> OTHER INFORMATION: n = A,T,C or G
     33 <400> SEQUENCE: 1
W--> 34 teececeet tittittit tittitnaa aggaagteee aetiggeeee ecaagnitga
W--> 35 agtcaagggc agatttgggn tcattgaacn tcacttccaa ggtcaaggat tctcatgctc
     36 agtttgcaag gagtgagatt acagtggcct gcacctggct tattttggta ttttaagtaa
     37 agacagggtt teaccatgtt ggecaggetg ttettgaaet cetgacetea agtgtteece
W--> 38 ntgcctcggg cctcccaaag tgctgggatt acaggcatga accaccatcc ccagcettct
                                                                                   300
     39 etettettaa taatggettt et atg tet the act tet ete ata eee tea ete
                                                                                   352
                                  Met Ser Phe Thr Ser Leu Ile Pro Ser Leu
     40
     41
                                   1
                                                    5
     43 tgt ttc tcc ttg act ctc cca ttc ctg ttt tgt tat ctt tct tta tgg
                                                                                   400
     44 Cys Phe Ser Leu Thr Leu Pro Phe Leu Phe Cys Tyr Leu Ser Leu Trp
                         1.5
                                               20
     47 ccg ttt ctt tct gct ttt ctg ttt atc act cgc tgg cta ctt gcc ttt
                                                                                   448
     48 Pro Phe Leu Ser Ala Phe Leu Phe Ile Thr Arg Trp Leu Leu Ala Phe
                     30
                                          35
     51 etc tet eta tte tet gte tet gte eet gtt tet tet gtt tea agt tea
     52 Leu Ser Leu Phe Ser Val Ser Val Pro Val Ser Ser Val Ser Ser Ser
53 45 50 55
    55 atg gtt ctc tgt ctc tat ctc tct gtt tct gcc tct ccg tct gtc ttt 56 Met Val Leu Cys Leu Tyr Leu Ser Val Ser Ala Ser Pro Ser Val Phe
                                                                                  544
                                  65
            60
                                                        70
     59 tgt ttc tot tgc atg cag ggc ccc ata otg tgg atc atg gca aat ctg
60 Cys Phe Ser Cys Met Gln Gly Pro Ile Leu Trp Ile Met Ala Asn Leu
                                                                                  592
                             80
                                                  85
     63 ago cag coo too gaa tit gio cto tig ggo tio too too tit ggt gag
                                                                                  640
     64 Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser Ser Phe Gly Glu
```

ENTERED

APR-4 2001

RAW SEQUENCE LISTING DATE: 03/19/2001 PATENT APPLICATION: US/09/781,880 TIME: 13:09:42

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03192001\1781880.raw

67 ctg eag gcc ctt ctg tat ggc ccc ttc ctc atg ctt tat ctt ctc gcc 68 Leu Gin Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu Tyr Leu Ala 69 110 115 120 71 ttc atg gag aca cac atc atc ata gtt atg gtc ata gct gac acc cac 736 72 Phe Met Gly Asn Thr 11e 11e 11e Val Met Val 11e Ala Asp Thr His 73 125 130 135 . 75 cta cat acc ccc atg tac ttc ttc ctg gac att ttc ctg gag 784 6 Leu Mis Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu 77 140 145 150 78 atc ttg gta acc atg atg ccc aug atg ctc tac gac ctg ttg 80 The Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu 81 155 160 170 83 gtc cac cac aaa gtc att acc ttc act ggc tag gtc cag ttc tac 84 Val Pro His Lys Val I1e Thr Phe Thr Gly Cys Met Val Gln Phe Tyr 85 175 180 185 87 ttc cac ttt tcc ctg qgg tcc act ctc ctc atc ctg aca gac atg 88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu I1e Leu Thr Asp Met 89 190 1915 91 qcc ctt gat cqc ttt gtg qcc att tgc cac cac ctg ctg tag gc act 220 20 215 95 ctg atg agc cg gct att gtg tcc act gtg cgc tag gca act 976 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gtg cca ctg gtg gcg gc gcg gc 1024 103 gat tac tgc cat ggc ggc gtc atc aca ctc tct ctc ca gc gtg gca 104 Asp Tyr Cys His Gly Gly Val 11e Asn His Phe Phe Cys Asp Asn Glu 205 255 260 265 107 cct ctc ctc acg gt ttg tac acc ctt ctc acc ctt ttc ttg gaa att ctg 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 113 285 290 295 1140 30 305 1150 307 1150 307 116 gac ttt ctc tat ggc tac atg act ctc act ctc acc ctc ctc ctc acc act gcc ctc ttc ctc acc acc acc acc ctc ttc ctc acc ac	6	5					95					100		•			105		
68 Leu Gln Ala Leu Teu Tyr Gly Pro Phe Leu Met Leu Tyr Leu Leu Ala 120 115 120 120 736 74 71 ttc atg gga aac acc atc atc ata gtt atg gtc ata gct gac acc cac 736 72 Phe Met Cly Asn Thr 1e 1le Ile Val Met Val 1le Ala Asp Thr His 127 120 130 135 75 cta cat aca cac cat gtac ttc ttc ctg ggc aat ttt toc ctg ctg gag 784 6 Leu His Thr Pro Met Tyr Phe Phe Leu Cly Asn Phe Ser Leu Leu Glu 77 140 145 150 150 150 170 145 150 160 165 170 170 180 181 181 181 181 181 181 181 181 18			ctq	caq	qcc	ctt	ctq	tat	ggc	ccc	ttc	ctc	atg	ctt	tat	ctt	ctc	gcc	688
110	6	8 .	Leu	Gln	Ala	Leu	Leu	Tyr	Gly	Pro	Phe	Leu	Met	Leu	Tyr	Leu	Leu	Ala	
72 Phe Met Gly Asn Thr Ile 11e 11e Val Met Val 11e Ala Asp Thr His 73 125 75 cta cat aca coc atg tac ttc ttc ctg ggc aat ttt tcc ctg gtg 76 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu 77 140 150 79 atc ttq gta acc atg act gca gtg ccc agg atg ctc tca gac ctg ttg 80 Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu 81 155 160 165 170 83 gtc ccc cac ana gtc att acc ttc act ggc tgc atg gtc cag ttc tac 84 Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr 85 175 180 185 87 ttc cac ttt tcc ctg ggg tcc acc tcc ttc ctc atc ctg aca gac atg 88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met 89 190 190 195 91 qcc ctt gat cqc ttt gtg gcc act tcc cac cac ctg cgc tat ggc act 92 Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr 93 205 210 225 92 626 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gta ccc act gc ct tcc tcc ga gcc ttt ctc 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 245 250 107 cct ctc ctg cag ttg fca tcc acc cac ttc ttc ttg gc cat st gac 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 250 265 107 cct ctc ctc gcag ttg tac tcc ttc gac act cgc ctg ttg gac act gac 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 250 265 107 cct ctc ctc gcag ttg tca tcc ttc gac act cgc ctg ttg gac act gaa 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 250 265 107 cct ctc ctc gcag ttg tca tcc tcc gac act cgc ctg ttg gac act gaa 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 250 265 107 cct ctc ctc gcag ttg tca tcc tcc gac act cgc ctg ttg gac act gaa 1120 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 250 265 107 cct ctc ctc gcag ttg tca tcc tcc gac act cgc ctg ttg gac act gaa 1120 120 Ala Ser Ser Cys Gly Eys Asp Ser Asp Thr Arg Leu Leu Glu Phe Trp 121 300 305 310 122 4 Leu Val Phe Ile Gly Tyr Ser Ser Thr Thr Val Leu Arg Ile Pro Ser 131 320 320 32								-	_										
130	7	1	ttc	atg	gga	aac	acc	atc	atc	ata	gtt	atg	gtc	ata	gct	gac	acc	cac	736
75 cta cat aca ccc atg tac tte tic ctg ggc aat tit tee ctg etg gag 76 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu 77 140 145 150 160 165 170 79 atc ttg gta acc atg act gca gtg ccc agg atg ctc tca gac etg ttg 80 The Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu 81 155 160 165 170 83 gtc ccc cac aaa gtc att acc ttc act ggc tgc atg gtc cag ttc tac 84 Val Pro His Lys Val The Thr Phe Thr Gly Cys Met Val Gln Phe Tyr 85 175 180 185 87 ttc cac tit tcc ctg qgg tcc acc tcc ttc ctc atc ctg aca gac atg 88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Thr Asp Met 89 190 195 200 91 qcc ctt gat cgc tit gtg gcc atc tgc cac cac act gcg ctat agg act gcc 92 Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr 93 205 210 215 95 ctg atg agc cgg gct atg gtg tc cac dtg ggt ggg ggt gcc tgg gac 96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gta ccc act ttc ttc etg gac atg His Leu 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 245 250 103 gat tac tgc cat gg ggc gtc atc aac cac ttc ttc ttg gac aat gac 104 Asp Tyr Cys His Gly Gly Val Ile Ash His Phe Phe Cys Asp Ash Glu 105 255 260 265 107 cct ctc ctq cag ttg tac agc ttg acc act ttc ttc ttg gac aat gac 1120 270 275 280 111 gac ttt ctg atg gcc ttg acc ttt gtc ctc acc ctg ttg gac ttc tgg 1168 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109 270 275 280 111 gac ttt ctg atg gcc ttg acc atg gc act gc gc gg atc cct tc 1168 Phe Trp 119 270 275 280 111 gac ttt ctg atg gcc ttg acc atg gc acc act gc gc gg atc cct 1264 119 20 20 20 20 20 20 20 20 20 20 20 20 20																			
76 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu Leu Glu 77 140 145 150 79 atc ttq gta acc atq act gca qtq ccc aqq atq ctc tca gac ctq ttq 832 80 Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu 81 155 160 170 83 qtc ccc cac aaa gtc att acc ttc act ggc tqc atq gtc cag ttc tac 84 Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr 85 175 180 185 87 ttc cac ttt tcc ctq qqq tcc acc tcc tcc ctc atc ctg aca gac atq 88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met 89 190 200 91 qcc ctt gat cqc ttt qtq qcc atc tqc cac cca ctq cqc tat qqc act 92 Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr 93 205 210 215 95 ctq atq agc cqg gct atq tqt gtc caq ctq gct gqq gct gcc tqq gca 96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atq gta ccc act gc ctc tcc ega gct cat ct 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 245 250 103 gat tac tgc cat gqc gqc gtc atc acc cac ttc ttc tgt gac aat gaa 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 255 260 265 107 cct ctc ctq cqc gt gtc acc act tgc ctc ttc tgq gac tct tgq 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109 270 275 111 gac ttt ctq atq gcc ttq acc ttt, gtc ctc acc tcc ttc ctq gat tcc tq 12 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 113 285 290 115 ctc act ctc tct atq gc tac ata gtg acc act gtg ctc ttc ctq gdq acc ccc 1264 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 330 123 ctq gtc ttc atc agc tac agt agt acc act ttc ttc tg tac agc acc ccc tcc 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 330 123 ctq gtc ttc atc agc tac agt agt acc act ttc ttc tg tac agc acc ccc tcc 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 330 123 ctq gtc ttc atc agc tac agt agt acc act ttc ttc tg tac agc acc tcc 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser	7	3			125					130					135				
77	7	5	cta	cat	aca	ccc	atg	tac	ttc	ttc	ctg	ggc	aat	ttt	tcc	ctg	ctg	gag	784
79 atc ttq gta acc atg act gca qtg ccc aqg atg ctc tca gac etg ttg 80 fle Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu 81 155 83 gtc ccc cac aaa gtc att acc ttc act ggc tgc atg gtc cag ttc tac 84 Val Pro His Lys Val fle Thr Phe Thr Gly Cys Met Val Gln Phe Tyr 85 7 ttc cac ttt tcc ctg qgg tcc acc tcc ttc ctc atc ctg aca gac atg 88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met 89 190 190 190 200 976 191 195 210 201 205 215 210 225 230 297 225 230 297 205 230 297 206 245 250 260 275 280 281 284 285 286 286 287 287 287 287 288 288 288 288 288 288	7	6.	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly	Asn	Phe	ser	ren	Leu	Glu	
80 The Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp Leu Leu 1155	7	7		140					145					150					
81 155	7	9	atc	ttq	gta	acc	atg	act	gca	gtg	ccc	ayg	atg	ctc	tca	gac	ctg	ttg	832
83 gtc ccc cac and gtc att acc ttc act ggc tgc atg gtc cag ttc tac 84 Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr 85 175 180 185 7 ttc cac ttt tcc ctg qgg tcc acc tcc ttc ctc atc ctg aca gac atg 88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met 89 190 200 91 qcc ctt gat cqc ttt gtg gcc atc tgc cac ctc ttc ctc atg aca gac atg 928 88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met 89 190 200 91 qcc ctt gat cqc ttt gtg gcc atc tgc cac cdc cdg cgc tat qgc act 976 92 Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr 93 205 210 215 95 ctg atg agc cgg gct atg tgt gtc cag ctg gct ggc ggc tgg gca 96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 245 250 103 gat tac tgc cat ggg ggc gtc atc acc act ttc ttc tgt gac aat gaa 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 255 260 265 107 cct ctc ctg cag ttg tca tcg tct gac act cgc ctg ttg gaa ttc tgg 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109 270 275 280 111 gac ttt ctg atg gcc ttg acc ttt, gtc ctc agc tcc ttc ctg gtg acc 112 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 13 285 290 295 115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg ctg ctg tg acc 116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Tle Pro Ser 117 300 305 305 310 119 gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tc cac ctc tc 1264 126 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 217 300 305 305 310 129 gcc aaa gct tcc ttc gtg caa gta agt acc atc ttc ttg tat gtc aga ct 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 325 330 1220 335 330 123 ctg gct ctc act ctg gtg caa gtc agt agt acc atc ttc ttg tat gtc aga ct 124 Leu Val Phe Tle Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro 125 335 340 1408 1408	8	0 .	lle	Leu	Val	Thr	Met	Thr	Ala	Val	Pro	Arg	Met	Leu	Ser	Asp	Leu	Leu	
84 Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln Phe Tyr 85	8	1	155					160					1.65					170	
175	8	3	gtc	ccc	cac	aaa	gtc	att.	acc	ttc	act	gge	tgc	atg	gtc	cag	ttc	tac	880
175	8	4 '	Val	Pro	His	Lys	Val	Ile	Thr	Phe	Thr	Gly	Cys	Met	Val	Gln	Phe	Tyr	
88 Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr Asp Met 89 190 195 200 91 qcc ctt gat cqc ttt gtg gcc atc tgc cac cac ctg cgc tat qgc act 92 Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr 93 205 210 95 ctg atg agc cgg gct atg tgt gtc cag ctg gct ggg gct gcc tgg gca 96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 245 250 103 gat tac tgc cat ggc ggc gtc atc acc cact ttc ttc tgt gac aat gaa 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 255 260 265 107 cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gac ttc tgg 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109 270 275 280 11.1 gac ttt ctg atg gcc ttg acc ttt. gtc cta agc tcc tcc gtg gt acc 1216 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 113 285 290 295 115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg egg atc ccc tct 1264 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Ggg atc ccc tct 1264 12 Asp Phe Leu Met Ala Leu Thr Phe Val Cys Ser Ser Phe Leu Val Thr 130 305 305 310 119 gcc agc agc tgc cag aag gct ttc tc ca act tgc ggg tct cac ctc 126 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 131 320 320 325 330 123 ctg gtc ttc atc ggc tac agt agt acc act ttt ctg tat gdc agg cct 124 Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro 125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg agg agg tc gtg gcc ttg gtg acc 128 Cly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr																			
99	8	7	ttc	cac	ttt	tec	ctg	qgg	tec	acc	tcc	ttc	ctc	atc	ctg	aca	gac	atg	928
99	8	8	Phe	His	Phe	Ser	Leu	Gly	ser	Thr	Ser	Phe	Leu	Ile	Leu	Thr	Asp	Met	
92 Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr Gly Thr 93 205 210 215 95 ctg atg age cgg gct atg tgt gtc cag ctg gct ggc tgg gca dc tgg gcd atg tgt gtc cag ctg gct ggc tgg gcc tgg gca 1024 96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 255 250 103 gat tac tgc cat ggc ggc gtc atc acc acc ttc ttc tgt gac aat gaa 1120 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 255 260 265 107 cct ctc ctq cag ttg tca tgc tct gac act cgc ctg ttq gaa ttc tgg 1168 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109 270 275 280 111 gac ttt ctg atg gcc ttg acc ttt gtc ser ser Phe Leu Val Thr 113 285 290 290 114 gac ttt ctc tat ggc tac ata gtg acc act gtg ctg ctg ctg ctg acc 295 115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg ctg ctg acc 295 116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser 117 300 5295 305 119 gcc agc agc tgc cag aag gct ttc tcc cac tgc ggg tct cac ctc aca 1312 1264 1275 300 5295 330 1280 310 1291 315 320 325 330 1292 315 ctg gtc ttc atc ggc tac agt agt acc atc ttt tct gt gtg acc 1360 1294 1295 1395 1395 1395 1395 1395 1395 1395 13																			
93	9	1 .	gee	ctt	gat	cqc	ttt	gtg	gcc	atc	tgc	cac	cca	ctg	cgc	tat	ggc	act	976
95 ctg atg agc cgg gct atg tgt gtc cag ctg gct ggg gct tgg gca 1024 96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 245 250 103 gat tac tgc cat ggc ggc gtc atc acc act ttc ttc tgt gac aat gaa 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 255 260 107 cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttq gaa ttc tgg 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109 270 275 280 111 gac ttt ctg atg gcc ttt gac ttt gtc ctc agc tct ctc ctg gtg acc 112 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 113 285 290 205 115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg egg atc ccc tct 116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Tle Pro Ser 117 300 305 305 119 gcc agc agc tgc cag ag gtt ttc tcc act tgc gtg tct cac ctc aca 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 330 123 ctg gtc ttc atc ggc tac agt agt acc act ttt ttc tgt gtg gcc ttg gtg acc 1240 Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro 125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc ttg ggc cttg gtg act 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr																			
96 Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala Trp Ala 97 220 225 230 99 gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235 240 245 250 103 gat tac tgc cat ggc ggc gtc atc aac cac ttc ttc tgt gac aat gaa 104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105 255 265 107 cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gac att tc tgg 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109 270 111 gac ttt ctg atg gcc ttg acc ttt gtc ctc agc tcc ttc ctg gtg acc 112 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 113 285 290 115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct 110 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 123 ctg gtc ttc atc ggc tac agt agt acc atc atc ttc ttg ttg tat gtc agg cct 1240 340 345 125 360 1360 1260 1370 1270 1380 365 370 1280 1390 365 370 129 gcc aga agct cac agt agt acc act gtg gtg tct cac ctc acc 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 330 123 ctg gtc ttc atc ggc tac agt agt acc atc ttc ttg ttg tat gtc agg cct 1360 1360 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	9	3			205					210					2.15				
97	9	5	etg	atg	agc	cgg	gct	atg	tgt	gtc	cag	ctg	get	ggg	gct	gcc	tgg	gca	1024
99 gct cct ttc cta gcc atg gta ccc act gtc ctc tcc cga gct cat ctt 100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 101 235	9	6	Leu	Met	Ser	Arg	Ala	Met	Cys	Val	Gln	Leu	Ala	Gly	Ala	Ala	Trp	Ala	
100 Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala His Leu 250	9	7		220					225					230					
101 235	9	9 1	gct	cct	ttc	cta	gcc	atg	gta	ccc	act	gtc	ctc	t.cc	cga	gct	cat	ctt	1072
103 gat tac tgc cat ggc gqc qtc atc aac cac ttc ttc tgt gac aat gaa 1120 104 Asp Tyr Cys His Gly Gly Val 11e Asn His Phe Phe Cys Asp Asn Glu 265 107 cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gat ttc tgg 1168 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 280 111 gac ttt ctg atg gcc ttg acc ttt gtc ctc agc tcc ttc ctg gtg acc 1216 112 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 285 115 ctc atc tcc tat ggc tac ata gtg acc act gtg cgg atc ccc tct 1264 116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Tle Pro Ser 177 300 305 305 310 119 gcc agc agc tgc cag ag gct ttc ca act tgc ggg tct cac act gtg cgg atc ccc tct 1264 110 Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 213 315 320 325 330 123 ctg gtc ttc atc ggc tac agt agt acc atc ttt ttc ttg tat gtc agg cct 1360 124 Leu Val Phe Tle Gly Tyr Ser Ser Thr Tle Phe Leu Tyr Val Arg Pro 345 125 ggc aaa gct cac tct gtg caa gtc agt agg gct ttt ctg ttg gcc ttg gtg acc 1408 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	1.	00	Ala	Pro) Phe	Leu	Ala	Met	. Val	Pro	Tha	· Val	. Leu	Ser	Arg	j Ala	His	Leu	
104 Asp Tyr Cys His Gly Gly Val Ile Asn His Phe Phe Cys Asp Asn Glu 105	1	0.1	235	,				240)				245					250	
105																			1120
107 cct ctc ctg cag ttg tca tgc tct gac act cgc ctg ttg gaa ttc tgg 1168 108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109	1	04	Asp	Туз	Cys	His	Gly	Gly	val	He	Asn	His	Phe	Phe	Cys	as As	Asn	Glu	
108 Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp 109	1	05					255	i				260)				265		
109																			1168
11.1 gac ttt ctg atg gcc ttg acc ttt gtc ctc agc tcc ttc ctg gtg acc 11.2 Asp Phe Leu Met A1a Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 11.3 285 290 295 11.5 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct 11.6 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser 11.7 300 305 310 11.9 gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca 12.0 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 12.1 315 320 335 12.3 ctg gtc ttc atc ggc tac agt agt acc act ttc tcg tat gtg ctg agc ct 13.60 12.4 Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro 13.5 335 340 345 12.7 ggc aaa gct cac tct gtg caa gtc agc agg aag gtc gtg gcc ttg gtg act 14.08 12.0 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	1	08	Pro	Lei	Let	Gln	Leu	ser	: Cys	ser	Asp	Tha	: Arg	Lei	Let	Glu	Phe	Trp	
112 Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu Val Thr 113 285 115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct 116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser 117 300 119 gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 123 ctg gtc ttc atc ggc tac agt agt acc act ttt ctg ggg tct tac agg agg 124 Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro 125 335 127 ggc aaa gct cac tct gtg caa gtc agc agg agg aag gtc gtg gcc ttg gtg act 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr																			
113																			1216
115 ctc atc tcc tat ggc tac ata gtg acc act gtg ctg cgg atc ccc tct 116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser 117 300 305 310 119 gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 330 123 ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct 1360 124 Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro 125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 1408 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	1.	12	Asp	Phe	Leu	Met	. Ala	Leu	Thr	Phe	· Va.i	Let	ser	Sei			Val	Thr	
116 Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile Pro Ser 117 300 305 310 119 gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca 1312 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 320 325 330 123 ctg gtc ttc atc ggc tac agt agt agt acc atc ttc tcg tat gtc agg cct 1360 124 Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val Arg Pro 125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 1408 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	1	13			285	5				290					295	5			
117 300 305 305 310 310 3112 312 320 320 420 420 420 420 420 420 420 420 420 4																			1264
119 gcc agc agc tgc cag aag gct ttc tcc act tgc ggg tct cac ctc aca 120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 123 ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct 124 Leu Val Phe Tle Gly Tyr Ser Ser Thr Tle Phe Leu Tyr Val Arg Pro 125 126 335 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	1	1.6	Leu	11.6	se.	r Tyr	Gly	тyr			Thi	Tha	· Val			, Ile	Pro	Ser	
120 Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr 121 315 123 ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct 124 Leu Val Phe Tle Gly Tyr Ser Ser Thr Tle Phe Leu Tyr Val Arg Pro 125 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr																			
121 315 320 325 330 123 ctg gtc ttc atc ggc tac agt agt acc atc tt ctg tat gtc agg cct 1360 124 Leu Val Phe Tle Gly Tyr Ser Ser Thr Tle Phe Leu Tyr Val Arg Pro 125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 1408 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr																			1312
123 ctg gtc ttc atc ggc tac agt agt acc atc ttt ctg tat gtc agg cct 124 Leu Val Phe Tle Gly Tyr Ser Ser Thr Tle Phe Leu Tyr Val Arg Pro 125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 128 Cly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr			A1 a	sei	: Ser	: Cys	Gln			Phe	ser	Thr			seı	: His	Leu		
124 Leu Val Phe Tie Gly Tyr Ser Ser Thr Tie Phe Leu Tyr Val Arg Pro 125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 1408 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr													325	,				330	
125 335 340 345 127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 1408 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr		21	315	,															
127 ggc aaa gct cac tct gtg caa gtc agg aag gtc gtg gcc ttg gtg act 1408 128 Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	1.	21 23	315 ctq	i jgt.o	e tto	ato	ggc	tac	agt	. agt	. acc	ato	ttt	cto	tat	gtic	agg	cct	1360
128 Cly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu Val Thr	1. 1.	21 23 24	315 ctq	i jgt.o	tto L Phe	ato	Gly	tac Tyr	agt	agt Ser	acc Thr	τ1.6	e Phe	cto Lev	tat Tyi	gtc val	. Arg	Pro	1360
	1. 1. 1.	21 23 24 25	315 ctg Leu	i gto Val	. Phe	e Ile	Gly 335	tac Tyr	agt Ser	Ser	Thr	11.e	e Phe	Leu	Туі	val	. Ang 345	Pro	
129 350 355 360	1. 1. 1.	21 23 24 25 27	315 ctg Leu	gto Val	. Phe	a Ile	Gly 335 tct	tac Tyr gtg	agt Ser	Ser	Thr agg	11.6 340 aag	e Phe) g gto	Lei gtg	gco	val	. Arg 345 1 gtg	Pro act	
	1. 1. 1. 1.	21 23 24 25 27 28	315 ctg Leu	gto Val	. Phe	t le cac His	335 tct ser	tac Tyr gtg	agt Ser	Ser	agg Arg	11.6 340 aag Lys	e Phe) g gto	Lei gtg	gco	r Val c ttg n Leu	. Arg 345 1 gtg 1 Val	Pro act	

RAW SEQUENCE LISTING DATE: 03/19/2001
PATENT APPLICATION: US/09/781,880 TIME: 13:09:42

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03192001\I781880.raw

						-											
131	tca	gtt	ete	acc	ccc	ttt	ctc	aat	ccc	ttt	atc	ctt	acc	ttc	tgc	aat	1456
								Asn									
133			365					370					375				
135	cag	aca	gtt	aaa	aca	gtg	cta	cag	ggg	cag	atg	cag	agg	ctg	aaa	ggc	1504
136	Gln	Thr	Val	Lys	Thr	Val	Leu	Gln	Gly	Glu	Met	Gln	Arg	Leu	Lys	Gly	
137		380					385					390					
							tgag	jece:	agg g	geeca	iggq	ga ac	cctqq	geet	3		1552
		CAR	Lys	Ala	Gln	*											
	395											_					1610
143	cct	ccatt	:ga c	cagt	tct	gt ge	gggag	gggag	y acc	ctcca	igea	agt	ggga	iga a	acacı	tgetga	1612
144	gtt	cttt	ag t	tttt	ttc	ec to	ctgag	gcaai	t aac	ctaca	igtg	age	cctga	agt s	derde	cactgt	1672 1732
145	etge	JCCC3	aaa c	ictei	tate	gg ac	ccace	catgo	g aaq	gagti	CCC	taca	tecc	oct i	ggcaq	geegta	1792
146	agaa	CCC	iga ç	jagta	igee	ca ga	aget	LCas	y Lak	aayyy	jaay	cyca	e cg cg	30C 1	raati	atttaa cgacgg	1852
								_ga c	3 aaq	gayyı	.ag L	cya	rgogg	JCC 9	geg co	gacgg	1875
	-		gat a EQ II	-		a al	Ly										1073
			ENGTI														
			PE:		, ,												
					Home	า รลเ	piens	=									
			EQUE			.,											
						Leu	Ile	Pro	ser	Leu	Cys	Phe	ser	Leu	Thx	Leu	
157	1				5					10	•				15		
1.58	Pro	Phe	Leu	Phe	Cys	Tyr.	Leu	Ser	Leu	Trp	Pro	Phe	Leu	Ser	Ala	Phe	
159				20	•	-			25					30			
160	Leu	Phe	ī l.e	Thr	Arg	Trp	Leu	Leu	Ala	Phe	Leu	ser	Leu	Phe	Ser	Val.	
161			35					40					45				
162	ser	۷al	Pro	Val	Ser	ser		ser	ser	Ser	Met		Leu	Cys	Leu	Tyr	
163		50					55					60				_	
		Ser	Val.	Ser	Ala		Pro	ser	Val	Phe		Phe	Ser	Cys	Met	Gin	
165						70			_	_	75				a.i.	80	
	Gly	Pro	He	Leu		116	Met	Ala	Asn		ser	GIn	Pro	ser	95	Pue	
167		-		a1	85	(1		Bha	C1	90	T 0.11	Cln	x 1 -	Lon		Mure.	
	Val.	Leu	Leu	-	Pne	ser	ser	Phe	105	G.Lu	rea	GIII	нла	110	neu	ıyı	
169	Clar	1) 20	Dho	100	Mot	Lou	TT 177	Leu		Λla	Dhe	Mot	Glv		Thr	Tle	
171	GTÄ	PLO	115	цея	MC C	neu	ıyı	120	пеп	niu	LIIC	1100	125	11011	2,111.		
	TIA	110		Met	Val	Tle	Ala	Asp	Thr	His	Leu	His		Pro	Met	Tyr	
173	11.0	130	, 41	1100	1 4.1		135	E				140					
	Phe		Leu	Glv	Asn	Phe		Leu	Leu	Glu	I.l.e	Leu	Val	Thr	Met	Thr	
	145	,				150					155					160	
176	Ala	Val.	Pro	Arq	Met	Leu	Ser	Asp	Leu	Leu	Val.	Pro	His	Lys	Val	lle	
1.77				,	165					170				-	1.75		
178	Thr	Phe	Thr	Gly	Cys	Met.	Val	Gln	Phe	Tyr	Phe	His	Phe	Ser	Leu	Gly	
179				180					185					190			
180	Ser	Thr	ser	Phe	ren	Tle	Leu	Thx	Asp	Met	Ala	Leu		Arg	Phe	Va l.	
181			195					200					205				
	Ala		Cys	His	Pro	Leu		Tyr	Gly	Thr	Leu		Ser	Arg	Ala	Met	
1.83		21.0					215					220				:	
184	Cys	Val	Gln	Leu	Ala	Gly	A.La	Ala	Trp	Ala	Ala	Pro	Phe	Leu	Ala	мес	

RAW SEQUENCE LISTING DATE: 03/19/2001 PATENT APPLICATION: US/09/781,880 TIME: 13:09:42

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03192001\1781880.raw

```
185 225
                         230
                                              235
                                                                    240
186 Val Pro Thr Val Leu Ser Arg Ala Nis Leu Asp Tyr Cys Nis Cly Gly
187 245 250 255
188 Val 11e Asn His Phe Phe Cys Asp Asn Glu Pro Leu Gln Leu Ser
189 260 265 270
190 Cys Ser Asp Thr Arg Leu Leu Glu Phe Trp Asp Phe Leu Met Ala Leu
191 275 280 285
192 Thr Phe Val Leu Ser Ser Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr
193 290 295 300
194 file Val Thr Thr Val Leu Arg file Pro Ser Ala Ser Ser Cys Gin Lys
195 305 310 315 320
196 Ala Phe Ser Thr Cys Gly Ser His Leu Thr Leu Val Phe Ile Gly Tyr
197 325 330 335
198 Ser Ser Thr Ile Phe Leu Tyr Val. Arg Pro Gly Lys Ala His Ser Val. 199 340 345 350
200 Gln Val Arg Lys Val Val Ala Leu Val Thr Ser Val Leu Thr Pro Phe
201 355 360 365
202 Leu Asn Pro Phe Ile Leu Thr Phe Cys Asn Gln Thr Val Lys Thr Val
203 370 375 380
204 Leu Gln Gly Gln Met Gln Arg Leu Lys Gly Leu Cys Lys Ala Gln
205 385 390
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1200
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 3
213 atglettica etteteteat acceteacte tgitteteet tgaeteteee atteetgitt
214 tgttatettt etttatggee gtttetttet gettttetgt ttateaeteg etggetaett
215 geetttetet etetattete tgtetetgte eetgtttett etgttteaag tteaatggtt
                                                                               240
216 etetytetet atetetetyt tretyeetet eegtetytet tittytitete tigeatyeag
217 ggccccatac tgtggatcat ggcaaatetg agccagecet cegaatttgt cetettggge
                                                                               300
                                                                               360
218 ttotoctoot tiggitgaget geaggeeett eigiaigee cetteeteat gettiatett
219 ctogoctica tgggaaacac catcatcata gttatggtca tagctgacac ccacctacat
                                                                               420
220 acaccoatgt acttetteet gggeaatttt teeetgetgg agatettggt aaccatgaet
                                                                               480
221 geagtgeeca ggatgetete agacetgttg gteececaca aagteattae etteactgge
                                                                               540
                                                                               600
222 tgeatgqtcc aqttctactt ccacttttcc ctggggtcca cetecttcct catectgaca
223 gacatggccc ttgatcgctt tgtggccatc tgccacccac tgcgctatgg cactctgatg
                                                                               660
224 ageogggeta tgtgtgteca getggetggg getgeetggg cageteettt eetageeatg
                                                                               780
225 gtacccactg tectotocog ageteatott gattactgcc atggeggegt catcaaccac
226 ttcttctgtg acaatgaacc tctcctgcag ttgtcatgct ctgacactcg cctgttggaa
                                                                               900
227 ttctgggact ttctgatggc cttgaccttt gtcctcagct ccttcctggt gaccctcatc
                                                                               960
228 tootatgget acatagtgae cactgtgetg eggateeect etgecageag etgecagaag
                                                                              1020
229 gettteteca ettgegggte teaceteaea etggtettea teggetaeag tagtaceate
230 tttctgtatg tcaggcctgg caaagctcac tctgtgcaag tcaggaaggt cgtggccttg
                                                                              1080
231 gtgacttcag ttctcacccc ctttctcaat ccctttatcc ttaccttctg caatcagaca
                                                                              1140
232 gttaaaacag tgctacaggg gcagatgcag aggctgaaag gcctttgcaa ggcacaatga
                                                                              1200
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 3630
236 <212> TYPE: DNA
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/781,880

DATE: 03/19/2001 TIME: 13:09:42

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03192001\1781880.raw

237	<213	8> OF	RGAN1	LSM:	Homo	sap	oiens	3									
239	<220)> FE	EATUE	RE:				/									
				KEY:													
				ION:		3)	(23)	34)									
243	<400)> S1	EQUE	ICE:	4						2000	auct	·act:	200	auac	teggee	: 60
244	gegt	10099	ice d	geege Faata	room	29 CC	og cog	cote	Logo	or Par	raaa	ecar	iacco	ret .	999c	ctyccy	120
243	otac	ayey	700 (rtice(rcage	an ar	ימפרני	at occ	ı acı	ictco	iaca - aaa	caga	agag	icc i	acca	ctgtga	180
247	acce	rtaca	rat a	accac	acce	ec ar	caco	acco	gaa	ıgaga	aacq	qqaq	1990	add	cgag	agagee	240
248	agag	agti	iac (qaqq	ccqq	ac ac	iccdd	cago	ge	gete	ccc	aggg	gaggg	gag	tceg	cagect	300
249	gage	itctt	ct o	ccaaq	gaaaa	ia aa	aaaa	igaaa	a aaa	aaaaa	aca	ac la	atg (gct	qca	aag	354
250															Al.a		
251.													1				
253	gag	aaa	ctg	gag	gca	gtg	tta	aat	gtg	gcc	ctg	agg	gtg	cca	agc	atc	402
		Lys	Leu	Glu	Ala		Leu	Asn	Val	Ala		Arg	Val	Pro	ser		
255	5					10			4		15		taa	* * *	* * * *	20	450
257	atg	ctg	ttg	gat	gtc	erg	tac	aga	Egg	gat	gue	age	cor	Dho	Pho	Cay	430
258	мес	ren	Leu	Asp	25	Leu	туг	Arg	rrp	30	Val	Ser	Ser	P IIC:	35		
	can	atro	caa	aga		age	ct t	agt	aat		cct	ett	tte	cag			498
262	Gln	Fle	Gln	Arg	Ser	Ser	Leu	Ser	Asn	Asn	Pro	Leu	Phe	Gln	Tyr	Lys	
263	01.11		0 3.13	40					45					50	•	-	
	tat	t.t.g	get	ctt	aat	atg	cat	tat	gta	ggt.	tat	atc	tta	agt	gtg	gtg	546
266	Tyr	Leu	Ala	Leu	Asn	Met	His	Tyr	Val	Gly	Tyr	11e	Leu	ser	Val	Val	
267			55					60					65				
269	ctg	cta	aca	ttg	CCC	agg	cag	cat	ctg	gtt.	cag	ctt	tat	cta	tat	ttt	594
	Leu		Thr	Leu	Pro	Arg		His	Leu	Va l	Gln		туг	Leu	Tyr	Phe	
271		70					75					80			~~~	+ - +	642
																tat Tyr	042
274	85	Thr	ATa	Leu	Leu	90	TAT	Ата	сту	nrs	95	116	36.1.	ALG	дзр	1.00	
		caa	agt	gaa	cta		+++	acc	tat	gag		cca	atq	tat	tta		690
				Glu													
279	,				105				_	110	-			•	115		
281	cct	ctc	tet	at.g	aat.	cgg	ttt	acc	aca	gcc	tta	ata	ggt	cag	ttg	gtg	738
282	Pro	Leu	ser	Met	Asn	Arg	Phe	Thr	Thr	Ala	Leu	lle	GľÀ	Gln	Leu	Val	
283				120					125					130			=0.0
285	gtg	tgt	act	tta	tgc	tec	tgt	gtc	atg	aaa	aca	aag	cag	att	tgg	ctg	786
	Val	Cys		Leu	Cys	ser	Cys		Met	Lys	Thr	Lys		He	Trp	Leu	
287			135					140	~+~	~~~	000	at a	145	att	at t	cot	834
289	Dho	CCa	get	cac	acg	Ton	Dro	Tan	Len	y Ca Ala	Ara	Len	Cve	Len	Val	cct Pro	054
290	PHE	150	Ala	HIS	met	rea	155	Беп	пен	MIG	ura	160	Cys	ucu	V C 1.	110	
	tta		aca	att	att	atic		aat.	aaa	ttt	qct.		att	ttt	act	gga	882
294	Leu	Glu	Thr	Ile	Val.	Ile	Ile	Asn	Lys	Phe	Ala	Met	Lle	Phe	Thr	Gly	
295	165					170					175					180	
297	ttg	gaa	gtt	ctc	tat	ttt	ctt	ggg	tct	aat	ctt	t.t.g	gta	cct	tat	aac	930
298	Leu	GLu	Val.	Leu	туг	Phe	Leu	Gly	ser	Asn	Leu	Leu	Val	Pro	Tyr:	Asn	
299					185					190					195		

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/781,880

DATE: 03/19/2001 TIME: 13:09:43

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03192001\I781880.raw

 $L\!:\!13\ M\!:\!270\ C\!:\!$ Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1